DETECTION OF NUCLEIC ACIDS BY TARGET-SPECIFIC HYBRID CAPTURE METHOD

FIELD OF INVENTION

This invention relates to the field of nucleic acid detection methods in general and more particularly relates to the detection of nucleic acids by target-specific hybrid capture method.

BACKGROUND OF THE INVENTION

The detection of specific nucleic acid sequences present in a biological sample is important for identifying and classifying microorganisms, diagnosing infectious diseases, detecting and characterizing genetic abnormalities, identifying genetic changes associated with cancer, studying genetic susceptibility to disease, and measuring response to various types of treatment. A common technique for detecting and quantitating specific nucleic acid sequences is nucleic acid hybridization.

Various hybridization methods are available for the detection and study of nucleic acids. In a traditional hybridization method, the nucleic acids to be identified are either in a solution or affixed to a solid carrier. The nucleic acids are detected using labelled nucleic acid probes which are capable of hybridizing to the nucleic acids. Recently, new hybridization methods have been developed to increase the sensitivity and specificity of detection. One example is the hybrid capture method described in U. S. Application Serial No. 07/792,585. Although these new hybridization methods offer significant improvements over the traditional methods, they still lack the ability to fully discriminate between highly homologous nucleic acid sequences.

It is therefore an object of the present invention to provide a hybridization method which is not only rapid and sensitive, but is also highly specific and capable of discriminating highly homologous nucleic acid target sequences.

SUMMARY OF THE INVENTION

The present invention provides a novel nucleic acid detection method, referred to herein as target-specific hybrid capture ("TSHC"). TSHC is a highly

specific and sensitive method which is capable of discriminating and detecting highly homologous nucleic acid target sequences.

In one embodiment, the method relates to detecting a target nucleic acid wherein the targeted nucleic acid is hybridized simultaneously, or sequentially, to a capture sequence probe and an unlabelled signal sequence probe. These probes hybridize to non-overlapping regions of the target nucleic acid and not to each other so that double-stranded hybrids are formed. The hybrids are captured onto a solid phase and detected. In a preferred embodiment, an DNA-RNA hybrid is formed between the target nucleic acid and the signal sequence probe. Using this method, detection may be accomplished, for example, by binding a labeled antibody capable of recognizing an DNA-RNA hybrid to the double-stranded hybrid, thereby detecting the hybrid.

In another embodiment, the signal sequence probe used in the detection method is a nucleic acid molecule which comprises a DNA-RNA duplex and a single stranded nucleic acid sequence which is capable of hybridizing to the target nucleic acid. Detection may be accomplished, for example, by binding a labeled antibody capable of recognizing the DNA-RNA duplex portion of the signal sequence probe, thereby detecting the hybrid formed between the target nucleic acid, the capture sequence probe and the signal sequence probe.

In yet another embodiment, the signal sequence probe used in the detection method is a molecule which does not contain sequences that are capable of hybridizing to the target nucleic acid. Bridge probes comprising sequences that are capable of hybridizing to the target nucleic acid as well as sequences that are capable of hybridizing to the signal sequence probe are used. In this embodiment, the signal sequence probe comprises a DNA-RNA duplex portion and a single stranded DNA sequence portion containing sequences complementary to sequences within the bridge probe. The bridge probe, which hybridizes to both the target nucleic acid and the signal sequence probe, therefore serves as an intermediate for connecting the signal sequence probe to the target nucleic acid and the capture sequence probe hybridized to the target nucleic acid.

In another embodiment of the TSHC method of the invention, blocker probes comprising oligonucleotides complementary to the capture sequence probes are

used in the method to eliminate excess capture sequence probe, thereby reducing the background signal in detection and increasing specificity of the assay.

The present invention also relates to novel probes. These probes are nucleic acid sequences which can function in various hybridization assays, including, for example, the TSHC assay.

BRIEF DESCRIPTION OF THE DRAWING

Figure 1 is a schematic diagram illustrating one embodiment of the target-specific hybrid capture method.

Figure 2 is a schematic diagram illustrating one embodiment of the target-specific hybrid capture method.

Figure 3 is a schematic diagram illustrating possible mechanisms of action of an embodiment that employs fused capture sequence probes in target-specific hybrid capture detection.

Figure 4 shows the analytical sensitivity and specificity of target-specific hybrid capture detection of HSV-1.

Figure 5 shows the analytical sensitivity and specificity of target-specific hybrid capture detection of HSV-2.

Figures 6A-6D show the various embodiments of the target-specific hybrid capture-plus method.

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides a method for detecting the presence of nucleic acids in test samples. More specifically, the invention provides a highly specific and sensitive method which is capable of discriminating and detecting highly homologous nucleic acid sequences.

Any source of nucleic acid, in purified or non-purified form, can be utilized as the test sample. For example, the test sample may be a food or agricultural product, or a human or veterinary clinical specimen. Typically, the test sample is a biological fluid such as urine, blood, plasma, serum, sputum or the like. Alternatively the test sample may be a tissue specimen suspected of carrying a nucleic acid of

interest. The target nucleic acid in the test sample may be present initially as a discrete molecule so that the sequence to be detected constitutes the entire nucleic acid, or may only be a component of a larger molecule. It is not necessary that the nucleic acid sequence to be detected be present initially in a pure form. The test sample may contain a complex mixture of nucleic acids, of which the target nucleic acid may correspond to a gene of interest contained in total human genomic DNA or RNA or a portion of the nucleic acid sequence of a pathogenic organism which organism is a minor component of a clinical sample.

The target nucleic acid in a test sample can be DNA or RNA, such as messenger RNA, from any source, including bacteria, yeast, viruses, and the cells or tissues of higher organisms such as plants or animals. Methods for the extraction and/or purification of such nucleic acids are well known in the art. Target nucleic acids may be double-stranded or single-stranded. In the present method, it is preferred that the target nucleic acids are single-stranded or made single-stranded by conventional denaturation techniques prior to the hybridization steps of the method. In a preferred embodiment, base denaturation technique is used to denature the double-stranded target DNA.

The term "oligonucleotide" as the term is used herein refers to a nucleic acid molecule comprised of two or more deoxyribonucleotides or ribonucleotides. A desired oligonucleotide may be prepared by any suitable method, such as purification from a naturally occurring nucleic acid, by molecular biological means, or by de novo synthesis. Examples of oligonucleotides are nucleic acid probes described herein.

Nucleic acid probes are detectable nucleic acid sequences that hybridize to complementary RNA or DNA sequences in a test sample. Detection of the probe indicates the presence of a particular nucleic acid sequence in the test sample. In one embodiment, the target-specific hybrid capture method employs two types of nucleic acid probes: capture sequence probe (CSP) and signal sequence probe (SSP). A capture sequence probe comprises a nucleic acid sequence which is capable of hybridizing to unique region(s) within a target nucleic acid and being captured onto a solid phase. A signal sequence probe comprises a nucleic acid sequence which is capable of hybridizing to regions within a target nucleic acid that are adjacent to the

unique regions recognized by the CSP. The sequences of CSP and SSP are selected so that they would not hybridize to the same region of a target nucleic acid or to each other.

In addition, the CSP and the SSP are selected to hybridize to regions of the target within 50, 000 bases of each other. The distance between the sequence to which the CSP hybridizes within the target nucleic acid and the sequence to which the SSP hybridizes is preferably between 1 to 50,000 bases, more preferably, the distance is less than 3,000 bases. Most preferably, the distance is less than 1,000 bases.

The CSP used in the detection method can be DNA, RNA, peptide nucleic acids (PNAs) or other nucleic acid analogues. PNAs are oligonucleotides in which the sugar-phosphate backbone is replaced with a polyamide or "pseudopeptide" backbone. In a preferred embodiment, the CSP is DNA. The CSP has a minimum length of 8 bases, preferably between 15 to 100 bases long, and more preferably between 20 to 40 bases long. The CSP is substantially complementary to the sequence within a target nucleic acid to which it hybridizes. The sequence of a CSP is preferably at least 75% complementary to the target hybridization region, more preferably, 100% complementary to this sequence. It is also preferred that the CSP contains less than or equal to 75% sequence identity, more preferably less than 50% sequence identity, to non-desired sequences believed to be present in a test sample. The sequence within a target nucleic acid to which a CSP binds is preferably 12 bases long, more preferably 20-40 bases long. It may also be preferred that the sequences to which the CSP hybridizes are unique sequences or group-specific sequences. Group-specific sequences are multiple related sequences that form discrete groups.

In one embodiment, the CSP used in the detection method may contain one or more modifications in the nucleic acid which allows specific capture of the probe onto a solid phase. For example, the CSP may be modified by tagging it with at least one ligand by methods well-known to those skilled in the art including, for example, nick-translation, chemical or photochemical incorporation. In addition, the CSP may be tagged at multiple positions with one or multiple types of labels. For example, the CSP may be tagged with biotin, which binds to streptavidin; or digoxigenin, which binds to anti-digoxigenin; or 2,4-dinitrophenol (DNP), which

binds to anti-DNP. Fluorogens can also be used to modify the probes. Examples of fluorogens include fluorescein and derivatives, phycoerythrin, allo-phycocyanin, phycocyanin, rhodamine, Texas Red or other proprietary fluorogens. The fluorogens are generally attached by chemical modification and bind to a fluorogen-specific antibody, such as anti-fluorescein. It will be understood by those skilled in the art that the CSP can also be tagged by incorporation of a modified base containing any chemical group recognizable by specific antibodies. Other tags and methods of tagging nucleotide sequences for capture onto a solid phase coated with substrate are well known to those skilled in the art. A review of nucleic acid labels can be found in the article by Landegren, *et al.*, "DNA Diagnostics-Molecular Techniques and Automation", Science, 242:229-237 (1988), which is incorporated herein by reference. In one preferred embodiment, the CSP is tagged with biotin on both the 5' and the 3' ends of the nucleotide sequence. In another embodiment, the CSP is not modified but is captured on a solid matrix by virtue of sequences contained in the CSP capable of hybridization to the matrix.

The SSP used in the detection method may be a DNA or RNA. In one particular embodiment of the invention, the SSP and target nucleic acid form a DNA-RNA hybrid. Therefore, in this embodiment, if the target nucleic acid is a DNA, then the preferred SSP is an RNA. Similarly, if the target nucleic acid is RNA, then the preferred SSP is a DNA. The SSP is generally at least 15 bases long. However, the SSP may be up to or greater than 1000 bases long. Longer SSPs are preferred. The SSP may comprise a single nucleic acid fragment, or multiple smaller nucleic acid fragments each of which is preferably between 15 to 100 bases in length.

In another embodiment, the SSP used in the detection method comprises a DNA-RNA duplex and a single stranded nucleic acid sequence capable of hybridizing to the target nucleic acid (Fig. 6A). The SSP may be prepared by first cloning a single stranded DNA sequence complementary to sequences within the target nucleic acid into a single-stranded DNA vector, then hybridizing RNA complementary to the DNA vector sequence to generate a DNA-RNA duplex. For example, if M13 is used as the DNA vector, M13 RNA is hybridized to the M13 DNA sequence in the vector to generate a DNA-RNA duplex. The resulting SSP contains a

DNA-RNA duplex portion as well as a single stranded portion capable of hybridizing to sequences within the target nucleic acid. The single stranded DNA should be at least 10 bases long, and may be up to or greater than 1000 bases long. Alternatively, the DNA-RNA duplex portion of the SSP may be formed during or after the reaction in which the single stranded portion of the SSP is hybridized to the target nucleic acid. The SSP can be linear, circular, or a combination of two or more forms. The DNA-RNA duplex portion of the SSP provides amplified signals for the detection of captured hybrids using anti-DNA-RNA antibodies as described herein.

In yet another embodiment, the SSP used in the detection method is a molecule which does not contain sequences that are capable of hybridizing to the target nucleic acid. In this embodiment, bridge probes comprising sequences capable of hybridizing to the target nucleic acid as well as sequences capable of hybridizing to the SSP are used. The bridge probes can be DNA, RNA, peptide nucleic acids (PNAs) or other nucleic acid analogues. In one embodiment (Fig. 6B), the SSP comprises a DNA-RNA duplex portion and a single stranded portion containing sequences complementary to sequences within the bridge probe. The bridge probe, which is capable of hybridizing to both the target nucleic acid and the SSP, therefore serves as an intermediate for connecting the SSP to the target nucleic acid and the CSP hybridized to the target nucleic acid. The SSP may be prepared as described above. In another embodiment (Fig. 6C), the SSP used in the detection method comprises multiple sets of repeat sequences as well as a single stranded RNA sequence capable of hybridizing to the bridge probe. A DNA oligonucleotide probe containing sequences complementary to the repeat sequences may be used to hybridize to the SSP to generate the RNA-DNA duplex needed for signal amplification. In yet another embodiment (Fig. 6D), the bridge probe contains a poly(A) tail in addition to sequences which are capable of hybridizing to the target nucleic acid. The SSP used in this example comprises poly(dT) DNA sequences. The bridge probe therefore is capable of hybridizing to the SSP via its poly(A) tail. A RNA probe comprising poly(A) sequences may be used to hybridize to the remaining poly(dT) DNA sequences within SSP to form a RNA-DNA duplex. The SSP comprising poly(dT)

sequences and the RNA probe comprising poly(A) sequences are preferably 100 to 5,000 bases long.

The SSP used in the detection method of the invention can be unmodified, or modified as with the CSP using methods described above and/or known in the art. In a preferred embodiment, the SSP is a covalently unmodified probe.

It is understood that multiple CSPs and/or SSPs can be employed in the detection method of the invention.

In another embodiment, an oligonucleotide probe comprising complementary sequences of two or more distinct regions of the target nucleic acid are fused together and used as the capture sequence probe in the method of the invention. Alternatively a single probe can be designed and produced which contains sequences complementary to single or multiple target nucleic acids. This type of probe is also referred to herein as a "fused" CSP. As shown in Example 5, the fused capture sequence probe works as effectively as the combination of two unfused CSPs when used at the same concentration.

The nucleic acid probes of the invention may be produced by any suitable method known in the art, including for example, by chemical synthesis, isolation from a naturally-occurring source, recombinant production and asymmetric PCR (McCabe, 1990 In: *PCR Protocols: A guide to methods and applications.* San Diego, CA., Academic Press, 76-83). It may be preferred to chemically synthesize the probes in one or more segments and subsequently link the segments. Several chemical synthesis methods are described by Narang et al. (1979 *Meth. Enzymol.* 68:90), Brown et al. (1979 *Meth. Enzymol.* 68:109) and Caruthers et al. (1985 *Meth. Enzymol.* 154:287), which are incorporated herein by reference. Alternatively, cloning methods may provide a convenient nucleic acid fragment which can be isolated for use as a promoter primer. A double-stranded DNA probe is first rendered single-stranded using, for example, conventional denaturation methods prior to hybridization to the target nucleic acids.

Hybridization is conducted under standard hybridization conditions well-known to those skilled in the art. Reaction conditions for hybridization of a

probe to a nucleic acid sequence vary from probe to probe, depending on factors such as probe length, the number of G and C nucleotides in the sequence, and the composition of the buffer utilized in the hybridization reaction. Moderately stringent hybridization conditions are generally understood by those skilled in the art as conditions approximately 25°C below the melting temperature of a perfectly base-paired double stranded DNA. Higher specificity is generally achieved by employing incubation conditions having higher temperatures, in other words more stringent conditions. Chapter 11 of the well-known laboratory manual of Sambrook et al., MOLECULAR CLONING: A LABORATORY MANUAL, second edition, Cold Spring Harbor Laboratory Press, New York (1990) (which is incorporated by reference herein), describes hybridization conditions for oligonucleotide probes in great detail, including a description of the factors involved and the level of stringency necessary to guarantee hybridization with specificity. Hybridization is typically performed in a buffered aqueous solution, for which conditions such as temperature, salt concentration, and pH are selected to provide sufficient stringency such that the probes hybridize specifically to their respective target nucleic acid sequences but not any other sequence.

Generally, the efficiency of hybridization between probe and target improve under conditions where the amount of probe added is in molar excess to the template, preferably a 2 to 10^6 molar excess, more preferably 10^3 to 10^6 molar excess. The concentration of each CSP provided for efficient capture is at least 25 fmoles/ml (25 pM) in the final hybridization solution, preferably between 25 fmoles to 10^4 fmoles/ml (10 nM). The concentration of each SSP is at least 15 ng/ml in the final hybridization solution, preferably 150 ng/ml. Table A shows the conversion of SSP concentrations expressed in ng/ml to molar basis.

Table A

Conversion of SSP Concentration From ng/ml to fmoles/ml

SSP Concentration in ng/ml	SSP Concentration in fmoles/ml (pM)	
	SSP is a 3kb RNA	SSP is a 5kb RNA
15 ng/ml	15.1	9
150 ng/ml	151	90
600 ng/ml	606	364

Hybridization of the CSP and the SSP to the target nucleic acid may be performed simultaneously or sequentially and in either order. In one embodiment, hybridization of the CSP and hybridization of the SSP to the target nucleic acid are performed simultaneously. The hybrid formed is then captured onto a solid phase coated with a substrate to which ligand attached to the CSP binds with specificity. In another embodiment, hybridization of the SSP to the target nucleic acid is performed after the hybridization of the CSP to the target nucleic acid. In this case, the CSP may be immobilized on a solid phase before or after hybridization. In this embodiment, both the CSP and the target may be bound to the solid phase during the SSP hybridization reaction.

It will be understood by those skilled in the art that a solid phase or matrix includes, for example, polystyrene, polyethylene, polypropylene, polycarbonate or any solid plastic material in the shape of plates, slides, dishes, beads, particles, cups, strands, chips and strips. A solid phase also includes glass beads, glass test tubes and any other appropriate glass product. A functionalized solid phase such as plastic or glass that has been modified so that the surface contains carboxyl, amino, hydrazide, aldehyde groups, nucleic acid or nucleotide derivatives can also be used. Any solid phase such as plastic or glass microparticles, beads, strips, test tubes, slides, strands, chips or microtiter plates can be used.

In one preferred embodiment, the CSP is labelled with biotin, and streptavidin-coated or avidin-coated solid phase is employed to capture the hybrid.

More preferably, streptavidin-coated microtiter plates are used. These plates may be coated passively or covalently.

The captured hybrid may be detected by conventional means well-known in the art, such as with a labelled polyclonal or monoclonal antibody specific for the hybrid, an antibody specific for one or more ligands attached to the SSP, a labelled antibody, or a detectable modification on the SSP itself.

One preferred method detects the captured hybrid by using an anti-RNA-DNA antibody. In this embodiment, the anti-RNA-DNA antibody is preferably labelled with an enzyme, a fluorescent molecule or a biotin-avidin conjugate and is non-radioactive. The label can be detected directly or indirectly by conventional means known in the art such as a colorimeter, a luminometer, or a fluorescence detector. One preferred label is, for example, alkaline phosphatase. Other labels known to one skilled in the art can also be employed as a means of detecting the bound double-stranded hybrid.

Detection of captured hybrid is preferably achieved by binding the conjugated antibody to the hybrid during an incubation step. Surfaces are then washed to remove any excess conjugate. These techniques are known in the art. For example, manual washes may be performed using either an Eppendorf™ Repeat Pipettor with a 50 ml Combitip™ (Eppendorf, Hamburg, Germany), a Corning repeat syringe (Corning, Corning, NY), a simple pump regulated by a variostat, or by gravity flow from a reservoir with attached tubing. Commercially available tube washing systems available from Source Scientific Systems (Garden Grove, CA) can also be used.

Bound conjugate is subsequently detected by a method conventionally used in the art, for example, colorimetry or chemiluminescence as described at Coutlee, *et al., J. Clin. Microbiol.* 27:1002-1007 (1989). Preferably, bound alkaline phosphatase conjugate is detected by chemiluminescence by adding a substrate which can be activated by alkaline phosphatase. Chemiluminescent substrates that are activated by alkaline phosphatase are well known in the art.

In another embodiment, the target specific hybrid capture method of the invention employs blocker probes in addition to the CSP and SSP. A blocker probe comprises sequences that are complementary to the sequences of the CSP. The

sequence of a blocker probe is preferably at least 75% complementary to the sequence of the CSP, more preferably, 100% complementary to the CSP. The addition of the blocker probes to the hybridization reaction mixture prevents non-hybridized CSP from hybridizing to cross-reactive nucleic acid sequences present in the target and therefore increases the specificity of the detection.

The blocker probe is generally at least 5 bases long, preferably 12 bases long. The concentration of the blocker probe in the hybridization reaction is preferably in excess to that of the CSP and SSP. Preferably, the blocker probe is present in a 2-fold molar excess, although, it may be present in an up to 10,000-fold molar excess. The blocker probes can be DNA, RNA, peptide nucleic acids (PNAs) or other nucleic acid analogues.

In one embodiment, blocker probes complementary to the full-length or near full-length of the CSP are used. Following the reaction in which the hybrid between CSP, SSP and the target nucleic acid is formed, one or more blocker probes may be added to the reaction and the hybridization is continued for a desired time. The hybridization products are then detected as described above.

In another embodiment, blocker probes complementary to only a portion of the CSP and are shorter than the CSP are used. These blocker probes have a lower melting temperature than that of the CSP. Preferably, the melting temperature of the blocker probe is 10 degrees lower than that of the CSP. In this case, the blocker probe is preferably added to the target nucleic acids simultaneously with the CSP and the SSP. Since the blocker probe has a lower melting temperature than the CSP, the initial temperature for hybridization is chosen such that the blocker probe does not interfere with the hybridization of the CSP to its target sequences. However, when the temperature of the hybridization mixtures is adjusted below the temperature used for target hybridization, the blocker probe hybridizes to the CSP and effectively blocks the CSP from hybridizing to cross-reactive nucleic acid sequences., For example, when the hybridization products are incubated at room temperature on a streptavidin-coated microtiter plate during hybrid capture, the blocker probes may be added.

The following examples illustrate use of the present amplification method and detection assay and kit. These examples are offered by way of

illustration, and are not intended to limit the scope of the invention in any manner. All references described herein are expressly incorporated *in toto* by reference.

Example 1

Target-Specific Hybrid Capture (TSHC) Assay Protocol

Herpes Simplex Virus 1 (HSV-1) and Herpes Simplex Virus 2 (HSV-2) viral particles of known concentration (Advanced Biotechnologies, Inc., Columbia, MD) or clinical samples were diluted using either Negative Control Media (Digene Corp., Gaithersburg, MD) or Negative Cervical Specimens (Digene). Various dilutions were made and aliquoted into individual microfuge tubes. A half volume of the Denaturation Reagent 5100-0431(Digene) was added. Test samples were incubated at 65°C for 45 minutes for denaturation of nucleic acids in the samples.

Following denaturation, a hybridization solution containing signal sequence probes (SSPs) (600 ng/ml each) and capture sequence probes (CSPs) (2.5 pmoles/ml each) was added to the sample, and incubated at 74°C for 1 hour. Blocker probes in a solution containing one volume of 4x Probe Diluent (Digene), one volume of Denaturation Reagent and two volumes of the Negative Control Media were then added to the hybridization mixture and incubated at 74°C for 15 minutes.

In a second series of experiments, following denaturation of nucleic acids, a hybridization mixture containing SSPs (600 ng/ml each), CSPs (2.5 pmoles/ml each), and blocker probes (250 pmoles/ml each) was added to the samples and incubated for one hour at 74°C.

Tubes containing reaction mixtures were cooled at room temperature for 5 minutes, and aliquots were taken from each tube and transferred to individual wells of a 96-well streptavidin capture plate (Digene). The plates were shaken at 1100 rpms for 1 hour at room temperature. The supernatants were then decanted and the plates were washed twice with SNM wash buffer (Digene) and inverted briefly to remove residual wash buffer. The alkaline-phosphatase anti-RNA/DNA antibody DR-1 (Digene) was then added to each well and incubated 30 minutes at room temperature. The wells were then subjected to multiple wash steps which include: 1) three washes with Sharp wash buffer (Digene) at room temperature; 2) incubation of

the plate with the Sharp wash buffer for 10 minutes at 60°C on a heat block; 3) two washes with the Sharp wash buffer at room temperature; and 4) one wash with the SNM wash buffer (Digene) at room temperature. Following removal of the residual liquid, luminescent substrate 5100-0350 (Digene) was added to each well and incubated for 15 minutes at room temperature. The individual wells were then read on a plate luminometer to obtain the relative light unit (RLU) signal.

Solutions containing Negative Control Media or known HSV Negative Cervical Specimens were used as negative controls for the test samples. The signal to noise ratio (S/N) was calculated as the ratio of the average RLU obtained from a test sample to the average RLU of the negative control. The signal to noise ratio was used as the basis for determining capture efficiency and the detection of target nucleic acids. A S/N value of 2 or greater was arbitrarily assigned as a positive signal while a S/N values less than 2 was considered negative. The coefficient of variation (CV) which is a determination of the variability of the experiment within one sample set was calculated by taking the standard deviation of the replicates, dividing them by the average and multiplying that value by 100 to give a percent value.

The capture sequence probes and the blocker probes used in experiments described in Examples 2-13 were synthesized using the method described by Cook et al. (1988 Nucl. Acid. Res., 16: 4077-95). Unless otherwise noted, the capture sequence probes used in the experiments described herein were labeled with biotins at their 5' and 3' ends.

The signal sequence probes used in experiments described in Examples 2-13 are RNA probes. These probes were prepared using the method described by Yisraeli et al. (1989, Methods in Enzymol., 180: 42-50).

Example 2

The following tables describe the various probes used in experiments described in Examples 3-13.

Table 1

HSV-1 Clones from which HSV-1 Probes are derived

Clone Name	Host Vector	Cloning Site(s)	Insert Size (bp)	Sequence Location within HSV-1
RH3	Dgx3	Hind III, Eco RI	5720	39850-45570
R10	Blue Script SK+	Eco RI	4072	64134-68206
RH5B	Blue Script SK+	Eco RV, Eco RI	4987	105108-110095
H19	Blue Script SK+	Hind III	4890	133467-138349

Table 2

HSV-2 Clones from which HSV-2 Probes are derived

Clone Name	Host Vector	Cloning Site(s)	Insert Size (bp)	Sequence Location in HSV-2
E4A	Blue Script SK+	Bam HI	3683	23230-26914
E4B	Blue Script SK+	Bam HI Eco RI	5600	26914-32267
I8	Blue Script SK+	Hind III	2844	41624-44474
EI8	Dgx3	Hind III, Eco RI	3715	44474-48189
4L	Blue Script KS+	Bam HI, Eco RI	4313	86199-90512

Table 3

Capture Sequence Probes for HSV-1

Probe	Sequence	Size (bp)	Location within HSV-1
TS-1	(TTATTATTA)CGTTCATGTCGGCAAACAGCT CGT(TTATTATTA) [SEQ ID NO:1]	24	105040-105063
TS-2	(TTATTATTA)CGTCCTGGATGGCGATACGGC (TTATTATTA) [SEQ ID NO:2]	21	110316-110336
VH-3	CGTCCTGGATGGCGATACGGC [SEQ ID NO:3]	21	110316-110336
NC-1	CGTTCATGTCGGCAAACAGCTCGT [SEQ ID NO:4]	24	105040-105063
VH-4 (fusion of VH3, NC-1)	CGTTCATGTCGGCAAACAGCTCGT-CGTCCTGGATGGCGATACGGC [SEQ ID NO:5]	45	105040-105063; 110316-110336
HZ-1	GATGGGGTTATTTTTCCTAAGATGGGGC GGGTCC [SEQ ID NO:6]	34	133061-133094
VH-2	TACCCCGATCATCAGTTATCCTTAAGGT [SEQ ID NO:7]	28	138367-138394
FD-1	AAACCGTTCCATGACCGGA [SEQ ID NO:8]	19	39281-39299
RA-2	ATCGCGTGTTCCAGAGACAGGC [SEQ ID NO:9]	22	39156-39177
NC-2	CAACGCCCAAAATAATA [SEQ ID NO:10]	17	46337-46353
FD-2	GTCCCCGAaCCGATCTAGCG (note small cap a is mutated base) [SEQ ID NO:11]	20	45483-45502
RA-4	CGAACCATAAACCATTCCCCAT [SEQ ID NO:12]	22	46361-46382
ON-3	CACGCCCGTGGTTCTGGAATTCGAC [SEQ ID NO:13]	25	64105-64129
HZ-2	(TTTATTA)GATGGGGTTATTTTTCCTAAGATG GGGCGGGTCC [SEQ ID NO:14]	34	133061-133094
ZD-1	GGTTATTTTTCCTAAG [SEQ ID NO:15]	16	133064-133079
ZD-2	(ATTATT)GGTTATTTTTCCTAAG(ATTATT) [SEQ ID NO:16]	16	133064-133079
F6R	ACGACGCCCTTGACTCCGATTCGTCATCGGAT GACTCCCT [SEQ ID NO:17]	40	87111-87150
BRH19	ATGCGCCAGTGTATCAATCAGCTGTTTCGGGT [SEQ ID NO:18]	32	133223-133254
F15R	CAAAACGTCCTGGAGACGGGTGAGTGTCGGC GAGGACG [SEQ ID NO:19]	38	141311-141348
VH-1	GTCCCCGACCCGATCTAGCG [SEQ ID NO: 20]	20	45483 - 45502
ON-4	GCAGACTGCGCCAGGAACGAGTA [SEQ ID NO: 21]	23	68404 - 68426
PZ-1	GTGCCCACGCCCGTGGTTCTGGAATTCGACAG CGA [SEQ ID NO: 22]	35	64105 - 64139
PZ-2	GCAGACTGCGCCAGGAACGAGTAGTTGGAGT ACTG [SEQ ID NO: 23]	35	68404 - 68438
FG-2	AAGAGGTCCATTGGGTGGGGTTGATACGGGA AAGAC [SEQ ID NO: 24]	36	105069 - 105104
FG-3	CGTAATGCGGCGGTGCAGACTCCCCTG [SEQ ID NO: 25]	27	110620 - 110646
FG-4	CCAACTACCCCGATCATCAGTTATCCTT AAGGTCTCTTG [SEQ ID NO: 26]	39	138362 - 138400

Hsv1-LF15R (SH-3)	(AAAAAAAAA)CAAAACGTCCTGGAGACGGGT GAGTGTCGGCGAGGACG [SEQ ID NO: 27]	38	141311-141348
Hsv1-F15-2B (GZ-1)	CAAAACGTCCTGGAGACGGGTGAGTGTCGGC GAGGACG [SEQ ID NO: 28]	38	141311-141348
Hsv1-F15-3B (GZ-2)	CAAAACGTCC-bio-U-GGAGACGGGTGAG TG-bio-U-CGGCGAGGACG [SEQ ID NO: 29]	38	141311-141348

* Sequences in parentheses are "tail" sequences not directed at HSV.

Table 4

Blocker Probes for HSV-1

Probe	Sequence	Size (bp)	Capture Probe to which it hybridizes
EA-1	AGGAAAAATAACCCCATC [SEQ ID NO:30]	18	HZ-1
EA-2	GACCCGCCCCATCTT [SEQ ID NO:31]	15	HZ-1
ZD-3	GGACCCGCCCCATCTTAGGAAAAATAAC CCCATC [SEQ ID NO:32]	34	HZ-1
NG-7	AAAAATAACCCCA [SEQ ID NO:33]	13	HZ-1
NG-8	CGCCCCATCTT [SEQ ID NO:34]	11	HZ-1
NG-4	CCATCTTAGGAAAAA [SEQ ID NO:35]	15	HZ-1
GP-1	ATAACTGATGATCGG [SEQ ID NO:36]	15	VH-Z
EA-3	CCACCCAATGGACCTC [SEQ ID NO: 37]	16	FG-2
EA-4	GTCTTTCCCGTATCAACC [SEQ ID NO: 38]	18	FG-2
EB-7	CGCCGCATTACG [SEQ ID NO: 39]	12	FG-3
EB-8	AGGGGAGTCTGC [SEQ ID NO:40]	12	FG-3
GP-3	CTGTTTGCCGACA [SEQ ID NO: 41]	13	VH-4
GP-4	TATCGCCATCCAG [SEQ ID NO: 42]	13	VH-4
EB-9	ATGATCGGGGTAGT [SEQ ID NO: 43]	14	FG-4
EB-10	AGAGACCTTAAGGATA [SEQ ID NO:44]	16	FG-4
NG-1	ATTCCAGAACCACGG [SEQ ID NO:45]	15	ON-3
NG-2	TTCCAGAACCACG [SEQ ID NO:46]	13	ON-3
NG-3	TCCAGAACCAC [SEQ ID NO:47]	11	ON-4
GP-5	GTTCCTGGCGCAG [SEQ ID NO: 48]	13	ON-4
GP-6	TTCCTGGCGCAG [SEQ ID NO: 49]	12	ON-4

Table 5

Capture Sequence Probes for HSV-2

Probe	Sequence	Size (bp)	Location within HSV-2
NF-1	GCCCGCGCCGCCAGCACTACTTTC [SEQ ID NO:50]	24	41610-41587
FG-1	AAACGTTGGGAGGTGTGTGCGTCATCCTG GAGCTA [SEQ ID NO:51]	35	48200-48234
LE-3	GACCAAAACCGAGTGAGGTTCTGTGT [SEQ ID NO:52]	26	48732-48757
NF-2	AAACGTTGGGAGGTGTGTGCGTCA [SEQ ID NO:53]	24	48200-48223
RA-3	TGCTCGTCACGAAGTCACTCATG [SEQ ID NO:54]	23	22756-22734

ON-2	CATTACTGCCCGCACCGGACC [SEQ ID NO:55]	21	23862-23842
LE-1	GCCGTGGTGTTCCTGAACACCAGG [SEQ ID NO:56]	24	27666-27643
LE-4	AGTCAGGGTTGCCCGACTTCGTCAC [SEQ ID NO:57]	25	22891-22867
NF-3	CAGGCGTCCTCGGTCTCGGGCGGGGC [SEQ ID NO:58]	26	32847-32822
NF-4	CCCACGTCACCGGGGGCCCC [SEQ ID NO:59]	20	26743-26724
LE-2	GCCGGTCGCGTGCGACGCCCAAGGC [SEQ ID NO:60]	25	33130-33106
SG-3	CCGACGCGTGGGTATCTAGGGGGTCG [SEQ ID NO: 61]	26	90559 – 90534
SG-4	CGGGACGGCGAGCGGAAAGTCAACGT [SEQ ID NO:62]	26	86194 – 86169

Table 6

Blocker Probes for HSV-2

Probe Name	Sequence	Size (bp)	Capture Probe to which it hybridizes
HX-4	GGCGCGGGC [SEQ ID NO:63]	9	NF-1
HX-5	GAAAGTAGTGCTGGC [SEQ ID NO:64]	15	NF-1
GP-7	TGCTGGCGGCG [SEQ ID NO:65]	11	NF-1
AZ-3	ACACCTCCCAACG [SEQ ID NO:66]	13	FG-1
AZ-4	CTCCAGGATGACG [SEQ ID NO:67]	13	FG-1
GR-1	TCGGTTTTGGTC [SEQ ID NO:68]	12	LE-3
GR-2	ACACAGAACCTCA [SEQ ID NO:69]	13	LE-3
GP-8	CACACACCTCCCA [SEQ ID NO:70]	13	NF-2
BR-10	CGACCCCCTAGATA [SEQ ID NO:71]	14	SG-3
BR-11	CCACGCGTCGG [SEQ ID NO:72]	11	SG-3
HX-6	ACGTTGACTTTCCGC [SEQ ID NO:73]	15	SG-4
BR-15	CGCCGTCCCG [SEQ ID NO:74]	10	SG-4

Table 7

Capture Sequence Probes for HPV

Probe	Sequence	Size (bp)	HPV Type and Sequence Location
ZL-1	GTACAGATGGTACCGGGGTTGTAGAAGTATCTG [SEQ ID NO:75]	33	HPV16 5360-5392
ZL-4	CTGCAACAAGACATACATCGACCGGTCCACC [SEQ ID NO:76]	31	HPV16 495-525
DP-1	GAAGTAGGTGAGGCTGCATGTGAAGTGGTAG [SEQ ID NO:77]	31	HPV16 5285-5315
DP-4	CAGCTCTGTGCATAACTGTGGTAACTTTCTGGG [SEQ ID NO:78]	33	HPV16 128-160
SH-1	GAGGTCTTCTCCAACATGCTATGCAACGTCCTG [SEQ ID NO:79]	33	HPV31 505-537
SH-4	GTGTAGGTGCATGCTCTATAGGTACATCAGGCC [SEQ ID NO:80]	33	HPV31 5387-5419
VS-1	CAATGCCGAGCTTAGTTCATGCAATTTCCGAGG [SEQ ID NO:81]	33	HPV31 132-164
VS-4	GAAGTAGTAGTTGCAGACGCCCCTAAAGGTTGC [SEQ ID NO:82]	33	HPV31 5175-5207
AH-1	GAACGCGATGGTACAGGCACTGCAGGGTCC [SEQ ID NO:83]	30	HPV18 5308-5337
AH-2	GAACGCGATGGTACAGGCACTGCA [SEQ ID NO:84]	24	HPV18 5314-5337
AL-1	ACGCCCACCCAATGGAATGTACCC [SEQ ID NO:85]	24	HPV18 4451-4474
PA-4	TCTGCGTCGTTGGAGTCGTTCCTGTCGTGCTC [SEQ ID NO:86]	32	HPV18 535-566
18-1AB	(TTATTATTA)CTACATACATTGCCGCCATGTTCG CCA [SEQ ID NO:87]	36	HPV18 1369-1395
18-2AB	(TTATTATTA)TGTTGCCCTCTGTGCCCCCGTTGT CTATAGCCTCCGT [SEQ ID NO:88]	46	HPV18 1406-1442
18-3AB	(TTATTATTA)GGAGCAGTGCCCAAAAGATTAAA GTTTGC [SEQ ID NO:89]	38	HPV18 7524-7552
18-4AB	(TTATTATTA)CACGGTGCTGGAATACGGTGAGG GGGTG [SEQ ID NO:90]	37	HPV18 3485-3512
18-5AB	(TTATTATTA)ACGCCCACCCAATGGAATGTACCC [SEQ ID NO:91]	33	HPV18 4451-4474
18-6AB	(TTATTATTA)ATAGTATTGTGGTGTGTTTCTCAC AT [SEQ ID NO:92]	35	HPV18 81-106
18-7AB	(TTATTATTA)GTTGGAGTCGTTCCTGTCGTG [SEQ ID NO:93]	30	HPV18 538-558
18-8AB	(TTATTATTA)CGGAATTTCATTTTGGGGCTCT [SEQ ID NO:94]	31	HPV18 634-655
PE-1	GCTCGAAGGTCGTCTGCTGAGCTTTCTACTACT [SEQ ID NO:95]	33	HPV18 811-843
PZ-2	GCGCCATCCTGTAATGCACTTTTCCACAAAGC [SEQ ID NO:96]	32	HPV45 77-108
PZ-5	TAGTGCTAGGTGTAGTGGACGCAGGAGGTGG [SEQ ID NO:97]	31	HPV45 5295-5325
CS-1	GGTCACAACATGTATTACACTGCCCTCGGTAC [SEQ ID NO:98]	32	HPV45 500-531

Probe	Sequence	Size (bp)	HPV Type and Sequence Location
CS-4	CCTACGTCTGCGAAGTCTTTCTTGCCGTGCC [SEQ ID NO:99]	31	HPV45 533-563
PF-1	CTGCATTGTCACTACTATCCCCACCACTACTTTG [SEQ ID NO:100]	34	HPV45 1406-1439
PF-4	CCACAAGGCACATTCATACATACACGCACGCA [SEQ ID NO:101]	32	HPV45 7243-7274
PA-1	GTTCTAAGGTCCTCTGCCGAGCTCTCTACTGTA [SEQ ID NO:102]	33	HPV45 811-843
45-5AB	(TTATTATTA)TGCGGTTTTGGGGGTCGACGTGGA GGC [SEQ ID NO:103]	36	HPV45 3444-3470
45-6AB	(TTATTATTA)AGACCTGCCCCCTAAGGGTACATA GCC [SEQ ID NO:104]	36	HPV45 4443-4469
45-8AB	(TTATTATTA)CAGCATTGCAGCCTTTTTGTTACT TGCTTGTAATAGCTCC [SEQ ID NO:105]	49	HPV45 1477-1516
45-9AB	(TTATTATTA)ATCCTGTAATGCACTTTTCCACAA A [SEQ ID NO:106]	34	HPV45 79-103
45-10AB	(TTATTATTA)GCCTGGTCACAACATGTATTAC [SEQ ID NO:107]	31	HPV45 514-535
45-11AB	(TTATTATTA)CAGGATCTAATTCATTCTGAGGTT [SEQ ID NO:108]	33	HPV45 633-656
ON-1	TGCGGTTTTGGGGGTCGACGTGGAGGC [SEQ ID NO:109]	27	HPV45 3444-3470

* Sequences in parentheses are "tail" sequences not directed at HSV.

Table 8

Blocker Probes For HPV

Probe	Sequence	Size (bp)	Capture Probe to which it hybridizes
PV-FD-1	GCCTCCACGTCGAC [SEQ ID NO:110]	14	ON-1/45-5AB
PV-FD-2	CCCCAAAACCG [SEQ ID NO:111]	11	ON-1/45-5AB
PV-FD-3	GGTACATTCCATTGGG [SEQ ID NO:112]	16	18-5AB/AL-1
PV-FD-4	TGGGCGTTAATAATAA [SEQ ID NO:113]	16	18-5AB
AH-3	ACCATCGCGTTC [SEQ ID NO:114]	12	AH-2
AH-4	GGACCCTGCAGTGC [SEQ ID NO:115]	14	AH-1
AH-5	CTGTACCATCGCGTT 3'[SEQ ID NO:116]	15	AH-1
AH-6	TGCAGTGCCTGT [SEQ ID NO:117]	12	AH-2
PZ-1	CCACCTCCTGCGT [SEQ ID NO:118]	13	PZ-5
PZ-3	ATTACAGGATGGCGC [SEQ ID NO:119]	15	PZ-2
PZ-4	GCTTTGTGGAAAAGTG [SEQ ID NO:120]	16	PZ-2
PZ-6	CCACTACACCTAGCACTA [SEQ ID NO:121]	18	PZ-5
ZL-2	CAGATACTTCTACAACC [SEQ ID NO:122]	17	ZL-1
ZL-3	CCGGTACCATCTGTAC [SEQ ID NO:123]	16	ZL-1
ZL-5	GGTGGACCGGTCG [SEQ ID NO:124]	13	ZL-4
ZL-6	ATGTATGTCTTGTTGCAG [SEQ ID NO:125]	18	ZL-4
DP-2	CTACCACTTCACATGC [SEQ ID NO:126]	16	DP-1
DP-3	AGCCTCACCTACTTC [SEQ ID NO:127]	15	DP-1

Probe	Sequence	Size (bp)	Capture Probe to which it hybridizes
DP-5	CCCAGAAAGTTACCAC [SEQ ID NO:128]	16	DP-4
DP-6	AGTTATGCACAGAGCT [SEQ ID NO:129]	16	DP-4
SH-2	CAGGACGTTGCATAGC [SEQ ID NO:130]	16	SH-1
SH-3	ATGTTGGAGAAGACCTC [SEQ ID NO:131]	17	SH-1
SH-5	GGCCTGATGTACCTATA [SEQ ID NO:132]	17	SH-4
SH-6	GAGCATGCACCTACAC [SEQ ID NO:133]	16	SH-4
VS-2	CTCGGAAATTGCATG [SEQ ID NO:134]	15	VS-1
VS-3	AACTAAGCTCGGCATT [SEQ ID NO:135]	16	VS-1
VS-5	GCAACCTTTAGGGG [SEQ ID NO:136]	14	VS-4
VS-6	CGTCTGCAACTACTACTTC [SEQ ID NO:137]	19	VS-4
CS-2	GTACCGAGGGCAGT [SEQ ID NO:138]	14	CS-1
CS-3	GTAATACATGTTGTGACC [SEQ ID NO:139]	18	CS-1
CS-5	GGCACGGCAAGAAA [SEQ ID NO:140]	14	CS-4
CS-6	GACTTCGCAGACGTAGG [SEQ ID NO:141]	17	CS-4
PF-2	CAAAGTAGTGGTGGG [SEQ ID NO:142]	15	PF-1
PF-3	GATAGTAGTGACAATGCAG [SEQ ID NO:143]	19	PF-1
PF-5	TGCGTGCGTGTATGTA [SEQ ID NO:144]	16	PF-4
PF-6	TGAATGTGCCTTGTGG [SEQ ID NO:145]	16	PF-4
PE-2	AGTAGTAGAAAGCTCAGC [SEQ ID NO:146]	18	PE-1
PE-3	AGACGACCTTCGAGC [SEQ ID NO:147]	15	PE-1
PA-2	TACAGTAGAGAGCTCGG [SEQ ID NO:148]	17	PA-1
PA-3	CAGAGGACCTTAGAAC [SEQ ID NO:149]	16	PA-1
PA-5	GAGCACGACAGGAACG [SEQ ID NO:150]	16	PA-4
PA-6	ACTCCAACGACGCAGA [SEQ ID NO:151]	16	PA-4

Example 3

Effect of the Extent of Biotin Labeling on Capture Efficiency

Tests were conducted to determine the optimal number of biotin labels per capture sequence probe for TSHC detection. The general TSHC method described in Example 1 was employed. The capture efficiency of capture sequence probe F15R labelled with one, two, or three biotins, measured by signal to noise ratio (S/N), were tested. The signal sequence probe employed was H19. As shown in Table 9, two biotins per capture sequence probe were sufficient for optimal capture efficiency. Greater than a 50% increase in S/N was observed using capture sequence probe with two biotin labels compared to the single biotin labeled capture sequence probe. The addition of a third biotin label to the capture sequence probe resulted in a decrease in S/N relative to the two-biotin labeled capture sequence probe.

Table 9

Effect of the Extent of Biotin Labeling on Capture Efficiency

# Biotins	*HSV-1/well*	*RLU*	*CV*	*S/N*
One	0	54	3%	1.0
One	4.5x10^3	236	2%	4.4
One	4.5x10^4	1861	3%	34.5
One	4.5x10^5	15633	7%	289.5
Two	0	46	3%	1.0
Two	4.5x10^3	296	10%	6.4
Two	4.5x10^4	2558	1%	55.6
Two	4.5x10^5	23369	4%	508.0
Three	0	44	22%	1.0
Three	4.5x10^3	243	6%	5.5
Three	4.5x10^4	1820	2%	51.4
Three	4.5x10^5	18581	8%	422.3

Example 4

Effect of the Distance between the CSP and the SSP Target Sites on Capture Efficiency

The effect of the distance between capture sequence probe (CSP) and signal sequence probe (SSP) hybridization sites on a HSV-1 target nucleic acid on capture efficiency was evaluated. CSPs that hybridize to HSV-1 nucleic acid sequences which are located 0.2kb, 3kb, 18kb, 36kb and 46kb from the site of SSP hybridization were tested. The general TSHC method described in Example 1 was employed. The capture efficiencies were 100%, 50%, 30%, 19% and 7%, respectively (Table 10). A steady decline in relative capture efficiencies was observed as the distance increased from 0.2 Kb to 46 Kb.

Table 10

Effect of Distance between Target Sites on Capture Efficiency

CSP	SSP	Distance Between Target Site	Relative Capture Efficiency
BRH19	H19	0.2 Kb	100%
F15R	H19	3 Kb	50%
F6R	RH5B	18 Kb	30%
F15R	RH5B	36 Kb	19%
F6R	H19	46 Kb	7%

Example 5

Effect of Fused Capture Sequence Probe on TSHC Detection of HSV-1

The binding capacity of streptavidin plates was determined to be approximately 2 pmoles of doubly-biotinylated CSPs per well. Since the CSPs are doubly biotin-labeled, a maximum of 8 CSPs (2 CSPs per SSP) is preferred in order not to exceed the binding capacity of the wells. Any increase in biotin-labeled capture sequence probe above the stated capacity resulted in a decrease in signal, the so-called "hook effect." In order to avoid this "hook effect" and still permit the use of greater than four SSP-CSP combinations, the effect of synthesizing oligonucleotides that contained the sequences of two CSPs fused together (5' and 3' sites) was tested. The fused capture sequence probes may function independently to drive hybridization to the unique target sites. In another embodiment, the fused probes may bind to two target sites with the second hybridization favored, since it is essentially a uni-molecular reaction with zero order kinetics once the probe has hybridized to the first site. The hybridization may be determined by one or both mechanisms. Previous experiments showed that two CSPs, VH3 and NC-1, when used together, gave approximately twice the S/N as the individual CSPs. Unfused capture sequence probes VH-3 and NC-1 were used at 2.5 pmoles/ml each for a total concentration of 5 pmoles/ml, fused probe VH-4 (fusion of VH-3 and NC-1) was used at 2.5 pmole/ml. As shown in Table 11, the fused probe was as effective as the combination of the two unfused probes. Therefore, TSHC detection using fused capture sequence probes permits the number of nucleic acid sequences targeted by the signal sequence probe to

be at least doubled without exceeding the plate biotin-binding capacity. The experiment also demonstrates the lack of cross-reactivity of HSV-2 at 10^7 genomes as shown by the S/N less than 2.0.

Table 11

Comparison of Fused v. Unfused Capture Sequence Probes in TSHC Detection of HSV-1

SSP	CSP	Viral Particles/ml	RLU	CV	S/N
RH5B	VH-3, NC-1	0	94	14%	1.0
RH5B	VH-3, NC-1	10^4 HSV-1	164	5%	1.7
RH5B	VH-3, NC-1	10^5 HSV-1	1003	4%	10.7
RH5B	VH-3, NC-1	10^7 HSV-2	125	6%	1.3
RH5B	VH-4 (fused)	0	97	10%	1.0
RH5B	VH-4 (fused)	10^4 HSV-1	181	3%	1.9
RH5B	VH-4 (fused)	10^5 HSV-1	1070	2%	11.0
RH5B	VH-4 (fused)	10^7 HSV-2	140	5%	1.4

Example 6

Capture Efficiency of Various CSPs and SSPs in TSHC Detection of HSV-1

The capture efficiency of capture sequence probes (CSPs) for each of the four HSV-1 specific signal sequence probes (SSPs), H19, RH5B, RH3 and R10, in the detection of HSV-1 by TSHC were evaluated. The criteria used for designing the capture sequence probes were: 1) the CSP hybridization site is within 1 kb either 5' or 3' of the SSP hybridization site on the HSV-1 nucleic acid sequence, preferably within 0.5 kb; and 2) the CSPs contain sequences that are unique to HSV-1, with no stretches of sequence homology to HSV-2 greater than 10 bases. The CSPs were designed to target the 5' and 3' regions adjacent to the SSP hybridization site, preferably with a 5' CSP and a 3' CSP for each SSP. The Omiga software (Oxford Molecular Group, Campbell, CA) was instrumental in the identification of such sites. The melting temperature (Tm) of the CSPs was designed to be between 70°C to 85°C, to conform to the 70°C to 75°C hybridization temperature used in Hybrid Capture II (HCII) assay for HSV (Digene). The general TSHC method described in Example 1 was employed. Eleven CSPs (which bind to 6 different sites) for H19, six CSPs (which bind to three unique sites) for RH5B, six CSPs (which bind to six unique sites) for RH3, and two

CSPs for R10 were tested. As shown in Table 12, efficient capture sequence probes were found for signal sequence probes H19, RH5B and R10.

Table 12

CSPs and SSPs for TSHC Detection of HSV-1

SSP	CSP	Cap%	SSP	CSP	Cap%	SSP	CSP	Cap%
R10	ON-3	100%	RH5B	TS-1	50%	H19	HZ-1	50%
R10	ON-3	80%	RH5B	NC-1	75%	H19	HZ-2	20%
			RH5B	VH-4	130%	H19	ZD-1	40%
			RH5B	TS-2	25%	H19	ZD-2	20%
			RH5B	VH-3	50%	H19	BRH19	70%
						H19	VH-2	70%
						H19	F15R	25%

Example 7

Capture Efficiency of Various CSPs and SSPs in TSHC Detection of HSV-2

The capture efficiency of capture sequence probes (CSPs) for each of the four HSV-2 specific signal sequence probes (SSPs), E4A, E4B, Ei8, and i8 , in the detection of HSV-2 by TSHC were evaluated. HSV-2 specific capture sequence probes (CSPs) were designed based on the same criteria as the HSV-1 CSPs except for the requirement that they be HSV-2 specific. Four CSPs for E4A, three CSPs for E4B, and two CSPs each for Ei8 and i8 were tested. The general TSHC method described in Example 1 was employed. As shown in Table 13, efficient capture sequence probes were found for i8 and Ei8.

Table 13

CSPs and SSPs for TSHC Detection of HSV-2

SSP	CSP	Cap%	SSP	CSP	Cap%
I8	NF-1	100%	Ei8	NF-2	50%
			Ei8	LE-3	45%

Example 8

Effect of Blocker Probes on HSV-1 and HSV-2 Detection

In an attempt to reduce cross-reactivity of TSHC while allowing the capture step to take place at room temperature, methods using blocker probes were developed. Blocker probes comprise sequences that are complementary to the capture sequence probes (CSPs) used for detection. These experiments were designed to prevent non-specific hybridization of the CSPs to non-targeted nucleic acids present in the sample under the lower stringency conditions, a situation often encountered during the room temperature capture step.

In one method, blocker probes that are complementary to the full length or nearly the full length of the capture sequences probe were used. The blocker probes were added to the reaction mixture in 10-fold excess relative to the CSP after hybridization of the CSP and the SSP to the target DNA molecule has occurred. Since the blocker probes have similar melting temperature as the CSPs, the CSPs were hybridized to the target nucleic acids first to prevent hybridization of the blocker probes to the CSPs before the hybridization of the CSPs to the target nucleic acids occurred. As shown in Table 14, the addition of the blocker probes resulted in a dramatic reduction in cross-reactivity while these probes had no effect on the sensitivity of HSV-1 detection. The S/N for the detection of cross-reactive HSV-2 (10^7 viral particles/ml) decreased from 5.0 to 0.8 when the blocker probes were used.

In another method, blocker probes that are complementary to only a portion of the CSPs and are shorter than the CSPs were used. The blocker probes were designed to have melting temperatures above room temperature but at least 10°C below the hybridization temperature of CSPs to the target nucleic acids. Since these blocker probes hybridize to the CSPs at temperature below the CSP hybridization

temperature to the target nucleic acids, the blocker probes may be added to the reaction at the same time as the CSP and SSP without effecting the hybridization efficiency of the CSPs to the target nucleic acid. These shorter blocker probes function during the room temperature capture step by hybridizing to the CSPs at the lower temperatures that are encountered during the room temperature capture step. As shown in Table 15, the addition of either single or paired shorter blocker probes in 100-fold excess relative to the CSPs resulted in a dramatic reduction in cross-reactivity but had no effect on sensitivity of HSV-1 detection. The S/N for detecting cross-reactive HSV-2 (10^7 viral particles/ml) without the blocker probes was 10.6, but was reduced to less than or equal to 1.5 with the addition of the blocker probes.

Therefore, both methods utilizing blocker probes provide a substantial reduction in cross-reactivity. The second method utilizing blocker probes with lower melting temperature may be preferred because the addition of blocker probes at the same time as the capture sequence probe eliminates the need for an extra step for the detection method.

Table 14

Effect of Blocker Probes Added Post Capture probe hybridization on TSHC

SSP	CSP	100x Blocker Probe	Viral Particles/ml	RLU	CV	S/N
H19	HZ-1	None	0	66	7%	1.0
H19	HZ-1	None	10^5 HSV-1	246	5%	3.7
H19	HZ-1	None	10^6 HSV-1	1998	2%	30.3
H19	HZ-1	None	10^7 HSV-2	327	2%	5.0
H19	HZ-1	ZD-3	0	60	3%	1.0
H19	HZ-1	ZD-3	10^5 HSV-1	267	4%	4.5
H19	HZ-1	ZD-3	10^6 HSV-1	2316	6%	38.6
H19	HZ-1	ZD-3	10^7 HSV-2	49	2%	0.8

Table 15

Effect of Blocker Probes Added Simultaneously with the Capture Probes on TSHC Detection of HSV-1

SSP	CSP	10x Blocker Probe	Viral Particle/ml	RLU	CV	S/N
H19	HZ-1	none	0	38	15%	1.0
H19	HZ-1	none	10^4 HSV-1	71	2%	1.9
H19	HZ-1	none	10^5 HSV-1	389	12%	10.2
H19	HZ-1	none	10^7 HSV-2	401	18%	10.6
H19	HZ-1	NG-4	0	39	8%	1.0
H19	HZ-1	NG-4	10^4 HSV-1	82	5%	2.1
H19	HZ-1	NG-4	10^5 HSV-1	411	18%	10.5
H19	HZ-1	NG-4	10^7 HSV-2	57	15%	1.5
H19	HZ-1	EA-1, EA-2	0	37	0%	1.0
H19	HZ-1	EA-1, EA-2	10^4 HSV-1	75	8%	2.0
H19	HZ-1	EA-1, EA-2	10^5 HSV-1	419	8%	11.3
H19	HZ-1	EA-1, EA-2	10^7 HSV-2	49	5%	1.3
H19	HZ-1	NG-7, NG-8	0	42	10%	1.0
H19	HZ-1	NG-7, NG-8	10^4 HSV-1	76	3%	1.8
H19	HZ-1	NG-7, NG-8	10^5 HSV-1	471	5%	11.2
H19	HZ-1	NG-7, NG-8	10^7 HSV-2	47	9%	1.1

Example 9

TSHC Detection Reduces Vector Background

The TSHC assay eliminates the vector contamination problem often associated with the Hybrid Capture II (HC II) detection assay (Digene). As the RNA signal sequence probes used in HC II are generated from linearized vector templates, any remaining unlinearized plasmid DNA results in the production of additional RNA probe sequences specific for vector sequences. In the HC II assay, the RNA/DNA hybrids that form as a result of these read-through transcripts are captured on the antibody coated plates and generate signal. In contrast, in the TSHC method, only those RNA/DNA hybrids that also hybridize to the capture sequence probes are detected. Accordingly, any detection of vector-related sequences is eliminated. Plasmids SK+, pBR322, DgZ and 1066 which were known to be detectable in HSV HC II test (Digene) were tested in the TSHC assay using two RNA signal sequence probes (H19 and RH5b) and two capture sequence probes (VH-2 and VH-4). Identical set of RNA probes were then used in HC II method and the TSHC method for the detection of HSV-1. The general TSHC method described in Example 1 was

employed. As shown in Table 16, while signal to noise ratio in standard HC II ranged from 14 to 48, the signal to noise ratio for the TSHC method was less than 2 for all plasmids tested.

Table 16

Vector Background in TSHC v. HCII Detection

Method	SSP	CSP	Targets/ml	RLU	CV	S/N
TSHC	H19 + RH5B	VH-2 + VH-4	0	94	6%	1.0
TSHC	H19 + RH5B	VH-2 + VH-4	4 ng pBS SK+	137	7%	1.5
TSHC	H19 + RH5B	VH-2 + VH-4	2 ng pBR322	99	6%	1.1
TSHC	H19 + RH5B	VH-2 + VH-4	4 ng DgX	135	7%	1.4
TSHC	H19 + RH5B	VH-2 + VH-4	4 ng 1066	107	7%	1.1
HC II	H19 + RH5B	None	0	94	9%	1.0
HC II	H19 + RH5B	None	4 ng pBS SK+	4498	3%	48.1
HC II	H19 + RH5B	None	2 ng pBR322	1281	8%	13.7
HC II	H19 + RH5B	None	4 ng DgX	2003	5%	21.4
HC II	H19 + RH5B	None	4 ng 1066	1536	2%	16.4

Example 10

Sensitivity and Specificity of detecting HSV-1 and HSV-2 by TSHC

The sensitivity and typing discrimination for the TSHC detection of HSV-1 and HSV-2 were assessed using the TSHC described in Example 1. In the HSV-1 TSHC assay, signal sequence probes H19 and RH5B, capture sequence probes HZ-1, VH-2 and VH-4, and blocker probes NG-7, NG-8, GP-3, GP-4, and GP-1 were used. In the HSV-2 TSHC assay, signal sequence probes I8 and Ei8, capture sequence probes NF-1 and NF-2, and blocker probes HX-4, HX-5 and GP-8 were used. HSV-1 and HSV-2 viral particles were diluted to various concentrations using the Negative Control Solution. As shown in Figures 4 and 5, while 10^4 copies of the either HSV-1 or HSV-2 (450 copies/well) were detected in the respective assays, there was virtually no detection of the cross-reactive type HSV at concentrations up to and including 10^8 copies/ml (4,500,000 copies/well). Thus, the HSV-1 and HSV-2 TSHC assays can

distinguish the two HSV types at a greater than 10,000-fold range of discrimination while maintaining excellent sensitivity (450 VP/well).

The HSV-1 TSHC assay shows a linear range of detection ranging from at least 2 x 10^3 to 5 x 10^3 VP/ml (Table 17). The specificity of the assay is excellent as no cross-reactivity was detected (S/N is less than or equal to 2) in samples containing HSV-2 at a concentration as high as 2 x 10^7 to 5 x 10^7 viral particles/ml. Similarly, the HSV-2 TSHC assay also shows excellent specificity, wherein no cross-reactivity was detected in samples containing HSV-1 at a concentration as high as 5 x 10^7 viral particles/ml (Table 18). Similar results were obtained from TSHC detection of HSV-2 using a dilution series of HSV-2 and HSV-1 viruses (Table 19).

Table 17

Analytical Sensitivity and Specificity of the HSV1 TSHC Assay

Targets	RLU	S/N
Negative Control	47	1.0
HSV2 @ 5x10^7 VP/ml	57	1.2
HSV2 @ 2x10^7 VP/ml	43	0.9
HSV1 @ 5x10^3 VP/ml	201	4.3
HSV1 @ 2x10^3 VP/ml	107	2.3

Table 18

Analytical Sensitivity and Specificity of the HSV2 TSHC Assay

Targets	RLU	S/N
Negative Control	40	1.0
HSV1 @ 5x10^7 VP/ml	78	2.0
HSV1 @ 2x10^7 VP/ml	55	1.4
HSV2 @ 5x10^3 VP/ml	218	5.5
HSV2 @ 2x10^3 VP/ml	106	2.7

Table 19

Detection with HSV-2 Probes using HSV-1 and HSV-2 of Different Dilution

Targets	RLU	S/N
Negative Control	43	1.0
HSV1 @ 5x10^7 VP/ml	112	2.6
HSV1 @ 2x10^7 VP/ml	57	1.3
HSV1 @ 1x10^7 VP/ml	38	0.9
HSV1 @ 1x10^6 VP/ml	38	0.9
HSV1 @ 1x10^5 VP/ml	33	0.8
HSV1 @ 1x10^4 VP/ml	52	1.2
HSV1 @ 1x10^3 VP/ml	43	1.0
HSV1 @ 1x10^2 VP/ml	39	0.9
HSV2 @ 1x10^7 VP/ml	257173	5980.8
HSV2 @ 1x10^6 VP/ml	28544	663.8
HSV2 @ 1x10^5 VP/ml	3200	74.4
HSV2 @ 1x10^4 VP/ml	266	6.2
HSV2 @ 5x10^3 VP/ml	181	4.2
HSV2 @ 1x10^3 VP/ml	62	1.4
HSV2 @ 1x10^2 VP/ml	44	1.0

Example 11

Clinical Specimen Testing

A 64-member clinical specimen panel was tested for HSV-1 and HSV-2 using both TSHC and HCII methods. The panel included 15 samples containing known quantities of HSV-1 or HSV-2, and 49 samples known to be negative for HSV-1 and HSV-2 by PCR testing. Accordingly, the 15 positive samples were "Expected" to test positive in both the HCII and TSHC assays, and the 49 negative samples were "Expected" to test negative in both the HCII and TSHC tests.

The general TSHC method described in Example 1 was employed. The results using the HCII method and the TSHC method are shown in Tables 20 and 21, respectively. Of the 49 samples "Expected" to yield negative result, 5 samples tested positive and 44 samples tested positive using the HCII method. In comparison, all 49

samples tested negative using the TSHC method. Therefore, the TSHC method is superior in specificity to the HCII method in the detection of HSV-1 and HSV-2.

Table 20

Observed vs. Expected Results for HCII Detection of HSV1 and HSV2

HCII Result	Expected Result	
	Positive	Negative
Positive	15	5
Negative	0	44
Total	15	49

Table 21

Observed vs. Expected Results for TSHC Detection of HSV1 and HSV2

TSHC Result	Expected Result	
	Positive	Negative
Positive	14	0
Negative	1	49
Total	15	49

Example 12

Effect of Combining Probes in TSHC Detection of HSV

The effect of combining HSV-1 specific signal sequence probe and capture sequence probe sets on HSV-1 detection was assessed. TSHC detection of HSV-1 and HSV-2 cross-reactivity was performed separately with two different sets of RNA signal sequence probe /biotinylated capture sequence probe combinations (Set #1: H19 plus HZ-1; and Set #2: RH5b plus the TS-1 and TS-2). TSHC was also performed with both RNA signal sequence probe/biotinylated capture sequence probe sets combined to assess the effect of combining the two probe sets on sensitivity and cross-reactivity. The general TSHC method described in Example 1 was employed. The results shown in Table 22 clearly demonstrate an additive effect of combining the two probe sets for HSV-1 detection with no apparent increase in HSV-2 cross-reactivity.

Table 22

Sensitivity is Improved by Combining HSV-1 Specific CSPs and SSPs

Capture Sequence Probes	Signal Sequence Probes	VP/ml	RLU	CV	S/N
HZ-1	H19	0	60	3%	1.0
HZ-1	H19	10^5 HSV-1	267	4%	4.5
HZ-1	H19	10^6 HSV-1	2316	6%	38.9
HZ-1	H19	10^7 HSV2	49	2%	0.8
TS-1, TS-2	RH5B	0	78	6%	1.0
TS-1, TS-2	RH5B	10^5 HSV-1	291	6%	3.8
TS-1, TS-2	RH5B	10^6 HSV-1	2368	11%	30.6
TS-1, TS-2	RH5B	10^7 HSV2	75	11%	1.0
HZ-1, TS-1, TS-2	H19, RH5B	0	70	12%	1.0
HZ-1, TS-1, TS-2	H19, RH5B	10^5 HSV-1	457	10%	6.5
HZ-1, TS-1, TS-2	H19, RH5B	10^6 HSV-1	4263	1%	60.9
HZ-1, TS-1, TS-2	H19, RH5B	10^7 HSV2	67	6%	1.0

Example 13

TSHC Detection of HPV18 and HPV45

The relative sensitivity and specificity of TSHC and HCII detection of Human Papillomavirus 18 (HPV18) and Human Papillomavirus 45 (HPV45) was compared. Previous studies have established HPV45 as the most cross-reactive HPV type to HPV18, and conversely, HPV18 as the most cross-reactive HPV type to HPV45. In this study, the ability of the two methods to detect HPV18 and HPV45 was assessed using HPV18 and HPV45 plasmid DNA.

Capture sequence probes (CSPs) for each of the four Human Papillomavirus types: HPV16, HPV18, HPV31, and HPV45, were designed. The criteria used for designing the capture sequence probes were: 1) the CSP hybridization istes do not overlap with the SSP sites; 2) the CSPs contain sequences unique to one HPV type with no stretches of sequence homology to other HPV types greater than 12 bases; and 3) the CSPs are of sufficient length so as to be capable of hybridizing efficiently at 70°C.

The blocker probes for each CSP were designed such that they could be added simultaneously with the CSP during hybridization to the target nucleic acid. The blocker probes have a melting temperature of at least 37°C but no higher than 60°C, as calculated by the Oligo 5.0 program (National Biosciences, Inc., Plymouth, MN). Two blocker probes were used for each capture oligonucleotide to maximize the blocker effect during the room temperature plate capture step. It was also desired that the blocker probes for each CSP have similar melting temperatures.

CSPs for each of the HPV types were tested for relative capture efficiency and cross-reactivity to other HPV types. CSPs that provided the best combination of sensitivity and low cross-reactivity were used for the detection of HPV using TSHC.

In TSHC and HCII detection of HPV18, HPV18 DNA was used at a concentration of 10 pg/ml. HPV45, used for cross-reactivity testing, was used at 4 ng/ml. The general TSHC method described in Example 1 was employed. As shown in Table 23, a signal to noise ratio of 16.9 was obtained for TSHC detection of HPV18 compared to a ratio of 7.6 obtained for HCII detection of HPV18. On the other hand, cross-reactivity with HPV45 was significantly reduced using the TSHC method (S/N of 1.3 for TSHC compared to S/N of 393.3 for HCII). The results clearly show that compared to the HCII method, the TSHC method for the detection of HPV18 was superior in both sensitivity and specificity. Results obtained in experiments comparing TSHC and HCII detection of HPV45 demonstrate that the TSHC method for the detection of HPV45 is superior in both sensitivity and specificity (Table 24).

Table 23

TSHC Detection of HPV 18

Method	Target	SSP	CSP	S/N
TSHC	0	18L1	18-7L	1.0
	HPV18 (10 pg/ml)	18L1	18-7L	16.9
	HPV45 (4 ng/ml)	18L1	18-7L	1.3
HC II	0	18L1	none	1.0
	HPV18 (10 pg/ml)	18L1	none	7.6
	HPV45 (4 ng/ml)	18L1	none	393.3

Table 24

TSHC Detection of HPV 45

Method	Target	SSP	CSP	S/N
TSHC	0	45L1	ON-1	1.0
	HPV45 (10 pg/ml)	45L1	ON-1	8.4
	HPV18 (4 ng/ml)	45L1	ON-1	1.6
HC II	0	45L1	none	1.0
	HPV45 (10 pg/ml)	45L1	none	8.2
	HPV18 (4 ng/ml)	45L1	none	494.0

Example 14

Target-Specific Hybrid Capture-Plus Assay Protocol

Hepatitis B Virus (HBV) was used as the model system for the development of the target-specific hybrid capture-plus (TSHC-plus) assay for the detection of target nucleic acids.

The hybridization in the TSHC-plus method (Fig. 6A-6D) may be performed in a single step. In the one-step method, CSPs, SSPs containing pre-hybridized DNA-RNA duplex, bridge probes (Fig. 6B-6D), and blocker probes are added simultaneously to the target nucleic acids. If hybridization is performed in two steps, CSPs, SSPs without pre-hybridized DNA-RNA duplex, bridge probes and blocker probes are first hybridized to the target nucleic acid. Oligonucleotide probes

complementary to the single stranded nucleic acid sequence in the SSP are then added to the reaction to form the DNA-RNA duplexes. The hybrids are then detected using anti-RNA/DNA antibody as described in Example 1.

Experiments were carried out to detect HBV using TSHC-plus (Examples 15-18). The method shown in Figure 6A was used. Human hepatitis B virus (HBV adw2) plasmid DNA of known concentration (Digene Corp) was diluted using HBV negative Sample Diluent (Digene). Various dilutions were made and aliquoted into individual tubes. The negative Sample Diluent was used as a negative control. A half volume of the Denaturation Reagent 5100-0431 (Digene) was added to the test samples. Test samples were incubated at 65° C for 45 minutes to denature the nucleic acids in the samples.

Following denaturation of the HBV sample, a hybridization solution containing capture sequence probes (CSPs), blocker probes, signal sequence probe comprising a M13 DNA/M13 RNA duplex and a single-stranded DNA sequence capable of hybridizing to HBV sequences was added to the samples, and incubated at 65° C for 1-2 hours. Alternatively, the denatured samples were incubated for 1 hour with a hybridization solution containing capture sequence probes (CSPs), blocker probes and M13 DNA plasmid containing HBV complementary sequences for 1 hour. Following the incubation, M13 RNA was added to the reaction and the incubation was continued for an additional hour at 65° C.

Tubes containing reaction mixtures were cooled at room temperature for 5 minutes and aliquots were taken from each tube and transferred to individual wells of a 96-well streptavidin plate (Digene). The plates were shaken at 1100 rpms for 1 hour at room temperature. The solution was then decanted and the plates were washed four times with SNM wash buffer (Digene). The alkaline-phosphatase anti-RNA/DNA antibody DR-I (Digene) was added to each well and incubated for 30 minutes at room temperature. The DR-1 (Digene) was then decanted and the plates were washed four times with SNM wash buffer (Digene). Following removal of the residual wash buffer, luminescent substrate (CDP-Star, Tropix Inc.) was added to each well and incubated for 15 minutes at room temperature. Individual wells were read on a plate luminometer to obtain relative light unit (RLU) signals.

Example 15

The following tables describe the various probes tested in the experiments described in Examples 16-18.

Table 25

Capture Sequence Probes for HBV

Probe	Sequence	Size (bp)	Location within HBV	Strand
HBV C1	GCTGGATGTGTCTGCGGCGTTTTATCAT (SEQ ID NO: 152)	28	374-401	Sense
HBV C2	ACTGTTCAAGCCTCCAAGCTGCGCCTT (SEQ ID NO: 153)	27	1861-1877	Sense
HBV C3	ATGATAAAACGCCGCAGACACATCCAGCG ATA (SEQ ID NO: 154)	32	370-401	Anti-sense

Table 26

HBV/M13 Clones from which SSPs are Prepared

Clone name	Vector	Cloning site	Insert Size (bp)	Location within HBV
SA1	M13 mp 18	Eco RI, Hind III	35	194-228
SA2	M13 mp 18	Eco RI, Hind III	34	249-282
SA1a	M13 mp 19	Eco RI, Hind III	35	194-228
SA2a	M13 mp 19	Eco RI, Hind III	34	249-282
SA4	M13 mp 19	Eco RI, Hind III	87	1521-1607

Table 27

HBV Blocker probes

Probe	Sequence	Size (bp)	CSP to which it hybridizes
B1	ATGATAAAACGCCG (SEQ ID NO: 155)	14	HBV C1
B2	CAGACACATCCAGC (SEQ ID NO: 156)	14	HBV C1
B3	AAGGCACAGCTTG (SEQ ID NO: 157)	13	HBV C2
B4	GAGGCTTGAACAGT (SEQ ID NO: 158)	14	HBV C2
B5	TATCGCTGGATGTGTC (SEQ ID NO: 159)	16	HBV C3
B6	TCGGCGTTTTATCATG (SEQ ID NO: 160)	16	HBV C3

Example 16

Effect of Blocker Probes on TSHC-Plus Detection of HBV

During room temperature capture step, excess SSP (M13 RNA/HBV-M13 DNA duplex) non-specifically hybridizing to the CSP are immobilized onto the plate which results in high background signals. In an attempt to reduce background signal, blocker probes were employed in TSHC-Plus detection of HBV. The blocker probes were designed to be much shorter than the CSPs so that they are only capable of hybridizing to the capture probes at temperatures well below the hybridization temperatures used in the assay.

Blocker probe sets consisting of two separate oligonucleotides that are complementary to the CSPs were used. The blocker probes were added to the hybridization mixture in 10-fold excess relative to the CSPs. Since the blocker probes are much shorter than the CSPs, they do not hybridize with CSPs at the target hybridization temperature and therefore do not interfere with the hybridization of the CSPs to the target nucleic acids. Following the hybridization of CSP and target nucleic acids, the samples were subjected to a room temperature capture step during which the blocker probes hybridize with excess CSPs, thus preventing them from hybridizing to the SSPs. As shown in Table 28, the use of the blocker probes in the hybridization reaction greatly reduced the background signals of the assay.

Table 28

Effect of Blocker Probes on HBV Detection

Capture Probe	Blocker probe	Background Signal (RLU)
HBV C1	no	17892
HBV C1	B1, B2	424
HBV C2	no	9244
HBV C2	B3, B4	398

Example 17

Effect of the Length of SSP on TSHC-Plus Detection of HBV

The effect of the length of the DNA sequence inserted into the M13 vector for generating the SSP on TSCH-Plus detection of HBV was studied. A

positive control containing 20 pg/ml of HBV plasmid DNA was used. As shown in Table 29, the use of a longer HBV complementary sequence in the SSP (87 base pairs) resulted in a substantial increase in signal of detection. The effect is unlikely due to sub-optimal hybridization temperature condition since the Tm of the shorter probes is 15 degree above the hybridization temperature. As the M13 RNA-DNA duplex formed in the SSP may act to partially block the complementary DNA sequence in the probe from hybridizing to the HBV sequences in the target nucleic acids, longer complementary sequences in the SSP may overcome this block.

Table 29

Effect of the Length of the Complementary sequence in the SSP on TSHC-Plus Detection of HBV

SSP	Size of the HBV Target DNA Sequence in SSP (bp)	Tm of the HBV Target DNA Sequence in SSP	Hybridization temperature	Signal (RLU)
SA1	35	83° C	65° C	1741
SA2	34	80° C	65° C	1857
SA4	87	108° C	65° C	7978

Example 18

TSHC-Plus and HC II Detection of HBV

The relative sensitivity of TSHC-Plus and HC II (Hybrid Capture II, Digene) detection of HBV was compared. HBV positive standards of three different concentrations were tested in the experiments. As shown in Table 30, the signals obtained using the TSHC-Plus detection method were approximately two-fold higher than those obtained using the HC II detection method.

Table 30

TSHC-Plus and HC II Detection of HBV*

Method	Control	Target HBV Concentration		
		10 pg/ml	20 pg/ml	100 pg/ml
HC II	48	2355	4225	21438
TSHC Plus	285	4856	7978	37689

* Signal measured as relative light unit (RLU)

The above description of various preferred embodiments has been presented for purposes of illustration and description. It is not intended to be exhaustive or limiting to the precise forms disclosed. Obvious modifications or variations are possible in light of the above teachings. The embodiments discussed were chosen and described to provide illustrations and its practical application to thereby enable one of ordinary skill in the art to utilize the various embodiments and with various modifications as are suited to the particular use contemplated. All such modifications and variations are within the system as determined by the appended claims when interpreted in accordance with the breadth to which they are fairly, legally and equitably entitled.